

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HILLMAN, JENNIFER L.  
CORLEY, NEIL C.  
PATTERSON, CHANDRA

(ii) TITLE OF INVENTION: HUMAN GLUTATHIONE PEROXIDASE-6

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: HEREWITH  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C  
(B) REGISTRATION NUMBER: 39,132  
(C) REFERENCE/DOCKET NUMBER: PF-0530 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-855-0572  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNOT20  
(B) CLONE: 1817518

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Val Ala Ala Thr Val Ala Ala Ala Trp Leu Leu Leu Trp Ala Ala
 1          5          10          15
Ala Cys Ala Gln Gln Glu Gln Asp Phe Tyr Asp Phe Lys Ala Val Asn
          20          25          30
Ile Arg Gly Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly Ser Val Ser
          35          40          45
Leu Val Val Asn Val Ala Ser Glu Cys Gly Phe Thr Asp Gln His Tyr
          50          55          60
Arg Ala Leu Gln Gln Leu Gln Arg Asp Leu Gly Pro His His Phe Asn
65          70          75          80
Val Leu Ala Phe Pro Cys Asn Gln Phe Gly Gln Gln Glu Pro Asp Ser
          85          90          95
Asn Lys Glu Ile Glu Ser Phe Ala Cys Arg Thr Tyr Ser Val Ser Phe
          100          105          110
Pro Met Phe Ser Lys Ile Ala Val Thr Gly Thr Gly Ala His Pro Ala
          115          120          125
Phe Lys Tyr Leu Ala Gln Thr Ser Gly Lys Glu Pro Thr Trp Asn Phe
          130          135          140
Trp Lys Tyr Leu Val Ala Pro Asp Gly Lys Val Val Gly Ala Trp Asp
145          150          155          160
Pro Thr Val Ser Val Glu Glu Val Arg Leu Gln Ile Thr Ala Leu Val
          165          170          175
Arg Lys Leu Ile Leu Leu Lys Arg Glu Asp Leu
          180          185

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## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
- (B) CLONE: 1817518

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GACGCCGCCA CCTCCGGAAC AAGCCATGGT GGCGGCGACG GTGGCAGCGG CGTGGCTGCT      60
CCTGTGGGCT GCGGCCTGCG CGCAGCAGGA GCAGGACTTC TACGACTTCA AGGCGGTCAA      120
CATCCGGGGC AAACCTGGTGT CGCTGGAGAA GTACCGCGGA TCGGTGTCCC TGGTGGTGAA      180
TGTGGCCAGC GAGTGC GGCT TCACAGACCA GCACTACCGA GCCCTGCAGC AGCTGCAGCG      240
AGACCTGGGC CCCCACCACT TCAACGTGCT CGCCTTCCCC TGCAACCAGT TTGGCCAACA      300
GGAGCCTGAC AGCAACAAGG AGATTGAGAG CTTTGCCCTGC CGCACCTACA GTGTCTCATT      360
CCCCATGTTT AGCAAGATTG CAGTCACCGG TACTGGTGCC CATCCTGCCT TCAAGTACCT      420
GGCCCAGACT TCTGGGAAGG AGCCACCTG GAACCTTCTGG AAGTACCTAG TAGCCCCAGA      480
TGGAAGGTG GTAGGGGCTT GGGACCCAAC TGTGTCAGTG GAGGAGGTCA GACTCCAGAT      540
CACAGCGCTC GTGAGGAAGC TCATCCTACT GAAGCGAGAA GACTTATAAC CACCGCGTCT      600
CCTCCTCCAC CACCTCATCC CGCCACCTG TGTGGGGCTG ACCAATGCAA ACTCAAATGG      660
TGCTTCAAAG GGAGAGACCC ACTGACTCTC CTTCCTTTAC TCTTATGCCA TTGGTCCCAT      720
CATTCCTGTG GGGGAAAAAT TCTAGTATTG TGATTATTG AATCTTACAG CAACAAATAG      780
GAACTCCTGG CCAATGAGAG CTCTTGACCA GTGAATCACC AGCCGATACG AACGTCTTGC      840
CAACAAAAAT GTGTGGCAAA TAGAAGTATA TCAAGCAATA ATCTCCCACC CAAGGCTTCT      900
GTAAACTGGG ACCAATGATT ACCTCATAGG GCTGTTGTGA GGATTAGGAT GAAATACCTG      960
TGAAAGTGCC TAGGCAGTGC CAGCCAAATA GGAGGCATTC AATGAACATT TTTTGCATAT     1020
AAACCAAAAA ATAACCTGTT ATCAATAAAA ACTTGCATCC AACATGAATT TC           1072

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GENBANK
- (B) CLONE: 544432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Cys	Ala	Ser	Arg	Asp	Asp	Trp	Arg	Cys	Ala	Arg	Ser	Met	His	Glu
1				5					10					15	
Phe	Ser	Ala	Lys	Asp	Ile	Asp	Gly	His	Met	Val	Asn	Leu	Asp	Lys	Tyr
			20					25					30		
Arg	Gly	Phe	Val	Cys	Ile	Val	Thr	Asn	Val	Ala	Ser	Gln	Cys	Gly	Lys
			35					40					45		
Thr	Glu	Val	Asn	Tyr	Thr	Gln	Leu	Val	Asp	Leu	His	Ala	Arg	Tyr	Ala
			50				55					60			
Glu	Cys	Gly	Leu	Arg	Ile	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly	Lys
65					70					75					80
Gln	Glu	Pro	Gly	Ser	Asn	Glu	Glu	Ile	Lys	Glu	Phe	Ala	Ala	Gly	Tyr
				85					90					95	
Asn	Val	Lys	Phe	Asp	Met	Phe	Ser	Lys	Ile	Cys	Val	Asn	Gly	Asp	Asp
			100					105					110		
Ala	His	Pro	Leu	Trp	Lys	Trp	Met	Lys	Ile	Gln	Pro	Lys	Gly	Lys	Gly
			115					120					125		
Ile	Leu	Gly	Asn	Ala	Ile	Lys	Trp	Asn	Phe	Thr	Lys	Phe	Leu	Ile	Asp
			130				135					140			
Lys	Asn	Gly	Cys	Val	Val	Lys	Arg	Tyr	Gly	Pro	Met	Glu	Glu	Pro	Leu
145					150					155					160
Val	Ile	Glu	Lys	Asp	Leu	Pro	His	Tyr	Phe						
				165					170						